

Shin-Lin Chen



OIPF

## RAW SEQUENCE LISTING

DATE: 05/19/2003

PATENT APPLICATION: US/09/925,548A

TIME: 11:18:37

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\05192003\I925548A.raw

```

4 1100 APPLICANT: Dedhar, Shukat
5      Hannigan, Greg
6      Yee, Arthur
8 1200 TITLE OF INVENTION: INTEGRIN-LINKED KINASE AND ITS USES
11 1300 FILE REFERENCE: KINE001CIE4
12 1400 CURRENT APPLICATION NUMBER: 09/925,548A
14 1410 CURRENT FILING DATE: 2001-08-08
16 1500 PRIOR APPLICATION NUMBER: 04/390,425
17 1510 PRIOR FILING DATE: 1999-09-08
19 1500 PRIOR APPLICATION NUMBER: 09/015,706
20 1510 PRIOR FILING DATE: 1998-03-05
22 1500 PRIOR APPLICATION NUMBER: 08/915,841
23 1510 PRIOR FILING DATE: 1997-10-31
25 1500 PRIOR APPLICATION NUMBER: 08/782,345
26 1510 PRIOR FILING DATE: 1996-11-19
28 1500 PRIOR APPLICATION NUMBER: 69/009,074
29 1510 PRIOR FILING DATE: 1995-12-21
31 1600 NUMBER OF SEQ ID NOS: 49
32 1700 SOFTWARE: FastSEQ for Windows Version 4.0
33 2100 SEQ ID NO: 1
36 2110 LENGTH: 1789
37 2120 TYPE: DNA
38 2130 ORGANISM: Homo sapiens
40 2400 SEQUENCE: 1
41  gattcatat gtgagatgat aacagggag tttcccgag aaggatcctg cagcccgagt      60
42  cccggggata aacttgggg ttcatccc cc tttccctg gat cactccacag tcttcagggt      120
43  tttcccaattc agtggactcg gggccgggac gctgct atg gac gac att ttc act      174
44  cag tgc cgg gag ggc aac gca gtc gcc gtt cgc ctg tgg ctg gac aac      210
45  aag gag aac gac ctg aac cag ggg gag gtt cat ggc ttc tcc ccc ttg      270
46  aac tgg ccc ttc tga gag ggt agc tct gct gtg gtt gag atg ttg atc      318
47  atg cgg ggg gca cgg atc aat gta atg aac cgt ggg gat gac aac ccc      366
48  ctg cat ctg gca gcc aat cat gga cac cgt gat att gta cag aag cta      414
49  ttg cag aac aag gca gac atc aat gca gtg aat gaa cac ggg aat gtg      462
50  ccc ctg cac tat gcc cgt tt tgg ggc caa gat caa gtg gca gag gac      510
51  ctg gtg gca aat ggg gcc att gtc agc atc tgt aac aag tat gga gag      558
52  atg cct gtg gac aaa gcc aac gca ccc ctg aga gag att ctc cga gag      606
53  cgg gca gaa aag atg gac cac aat ctc aac cgt att cca tac aag gac      654
54  aca ttc tgg aag ggg acc acc ggc acc cgg ccc cga aat gga acc ctg      702
55  aac aaa cac tct ggc att gac ttc aaa cag att aac ttc ctg aag aag      750
56  ctc aac gag aat cac tct gga gat cta tgg aag ggc cgc tgg cag ggc      798
57  aat gac att gtc gtg aag gtg ctg aag gtt cga gac tgg agt aca agg      846
58  gag agc agg gac ttc aat gaa gag tgt ccc cgg ctc agg att ttc tgg      894
59  aat cca aat gtg ctc cca gtg cta ggt gcc tgc cag tct cca cct gct      942

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60 cct cat cct act ctc atc aca cac tgg atg cgg tat gga tcc ctg tac      990
61 aat gta cta cat gaa ggc acc aat ttc gtc gtg gac cag agc bag gct      1000
62 gtg aag ttt gct tlg gac atg gaa agg ggc atg gcc ttc cta cac aca      1050
63 cta gag ccc ctg ctg cca cga cat gaa ctg aat agc cgt agt gta atg      1100
64 att gat gag gac atg act gcc cga att agc atg gct gat gtc aag ttc      1150
65 tct ttc caa tgt cct ggt cgc atg tat gaa cct gcc tgg gta gcc ccc      1200
66 gaa cct ctg cag aag aag cct gaa gac aca aac aga cgc tca gca gac      1250
67 atg tgg agt ttt gca gtg ctt ctg tgg gaa ctg gtg aca cgg gag gta      1300
68 ccc tct gct gac ctg tcc aat atg gag att gga atg aag gtg gca ttg      1350
69 gaa agc ctt cgg cct acc atc cca cca ggt att tcc cct cat gtg tgt      1400
70 aag ctg atg aag atc tgc atg aat gaa gac cct gca aag cga ccc aaa      1450
71 ttt gac atg att gtg cct atc ctt gag aag atg cag gac aag      1500
72 taggactgga aggtccttgc ctgaactcca gaggtgtcgg gacatgcttg ggggaatgca      1550
73 cctcccccaca ggaagcaggcc tctggttgcc tccccggcct ccagtcctgg tactacccca      1600
74 gctcgggggtc cctcccttcc ccccatccct accactgtgc gcaagagggg cgggtccaga      1650
75 gcttctgtcac tggccacatg gtgtctccca acatgggagg gatcagcccc gctgtccaca      1700
76 ataaagttta ttatgaaaaa aaaaaaaaaa aaaaaaa      1750
77 -210- SEQ ID NO: 2
78 -211- LENGTH: 452
79 -212- TYPE: PRT
80 -213- ORGANISM: Homo sapiens
81 -240- SEQUENCES: 2
82 Met Asp Asp Ile Phe Thr Gln Cys Arg Glu Gly Asn Ala Val Ala Val
83 1 5 10 15
84 Arg Leu Trp Leu Asp Asn Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp
85 20 25 30
86 His Gly Phe Ser Pro Leu His Trp Ala Cys Arg Glu Gly Arg Ser Ala
87 35 40 45
88 Val Val Glu Met Leu Ile Met Arg Gly Ala Arg Ile Asn Val Met Asn
89 50 55 60
90 Arg Gly Asp Asp Thr Pro Leu His Leu Ala Ala Ser His Gly His Arg
91 65 70 75 80
92 Asp Ile Val Gln Lys Leu Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val
93 85 90 95
94 Asn Glu His Gly Asn Val Pro Leu His Tyr Ala Cys Phe Trp Gly Gln
95 100 105 110
96 Asp Gln Val Ala Glu Asp Leu Val Ala Asn Gly Ala Leu Val Ser Ile
97 115 120 125
98 Cys Asn Lys Tyr Gly Glu Met Pro Val Asp Lys Ala Lys Ala Pro Leu
99 130 135 140
100 Arg Glu Leu Leu Arg Glu Arg Ala Glu Lys Met Gly Gln Asn Leu Asn
101 145 150 155 160
102 Arg Ile Pro Tyr Lys Asp Thr Phe Trp Lys Gly Thr Thr Arg Thr Arg
103 165 170 175
104 Pro Arg Asn Gly Thr Leu Asn Lys His Ser Gly Ile Asp Phe Lys Gln
105 180 185 190
106 Leu Asn Phe Leu Thr Lys Leu Asn Glu Asn His Ser Gly Glu Leu Trp
107 195 200 205
108 Lys Gly Arg Trp Gln Gly Asn Asp Ile Val Val Lys Val Leu Lys Val

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113      210      215      220
112 Arg Asp Trp Ser Thr Arg Lys Ser Arg Asp Phe Asn Glu Glu Cys Pro
114 225      230      235      240
115 Arg Leu Arg Ile Phe Ser His Pro Asn Val Leu Pro Val Leu Gly Ala
116      245      250      255
117 Cys Gln Ser Pro Pro Ala Pro His Pro Thr Leu Ile Thr His Trp Met
118      260      265      270
119 Pro Tyr Gly Ser Leu Tyr Asn Val Leu His Glu Gly Thr Asn Phe Val
120      275      280      285
121 Val Asp Gln Ser Gln Ala Val Lys Phe Ala Leu Asp Met Ala Arg Gly
122      290      295      300
123 Met Ala Phe Leu His Thr Leu Gln Pro Leu Ile Pro Arg His Ala Leu
124 305      310      315      320
125 Asn Ser Arg Ser Val Met Ile Asp Glu Asp Met Thr Ala Arg Ile Ser
126      325      330      335
127 Met Ala Asp Val Lys Phe Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala
128      340      345      350
129 Pro Ala Trp Val Ala Pro Gln Ala Leu Gln Lys Lys Pro Glu Asp Thr
130      355      360      365
131 Asn Arg Arg Ser Ala Asp Met Trp Ser Phe Ala Val Leu Leu Trp Glu
132      370      375      380
133 Leu Val Thr Arg Glu Val Pro Phe Ala Asp Leu Ser Asn Met Glu Ile
134 385      390      395      400
135 Gly Met Lys Val Ala Leu Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly
136      405      410      415
137 Ile Ser Pro His Val Cys Lys Leu Met Lys Ile Cys Met Asn Glu Asp
138      420      425      430
139 Pro Ala Lys Arg Pro Lys Phe Asp Met Ile Val Pro Ile Leu Glu Lys
140      435      440      445
141 Met Gln Asp Lys
142      450

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145 &lt;110&gt; SEQ ID NO: 3

146 &lt;111&gt; LENGTH: 19

147 &lt;112&gt; TYPE: DNA

148 &lt;113&gt; ORGANISM: Homo sapiens

149 &lt;400&gt; SEQUENCE: 3

151 agtccatagc aggtcccg

19

153 &lt;110&gt; SEQ ID NO: 4

154 &lt;111&gt; LENGTH: 18

155 &lt;112&gt; TYPE: DNA

156 &lt;113&gt; ORGANISM: Homo sapiens

158 &lt;400&gt; SEQUENCE: 4

159 aacatggtag cagtggac

18

161 &lt;110&gt; SEQ ID NO: 5

162 &lt;111&gt; LENGTH: 19

163 &lt;112&gt; TYPE: DNA

164 &lt;113&gt; ORGANISM: Homo sapiens

166 &lt;400&gt; SEQUENCE: 5

167 cctttccgg ggaactccc

19

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Input Set : D:\seqlist.txt

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169 <210> SEQ ID NO: 6
170 <211> LENGTH: 19
171 <212> TYPE: DNA
172 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 6
175 ggggactcag gctacaggc 19
177 <210> SEQ ID NO: 7
178 <211> LENGTH: 19
179 <212> TYPE: DNA
180 <213> ORGANISM: Homo sapiens
182 <400> SEQUENCE: 7
183 ggtttatctc cgggactcc 19
185 <210> SEQ ID NO: 8
186 <211> LENGTH: 19
187 <212> TYPE: DNA
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 8
191 ggggagggag atgagaccc 19
193 <210> SEQ ID NO: 9
194 <211> LENGTH: 19
195 <212> TYPE: DNA
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 9
199 ggcctgaggc tgtcagagta 19
201 <210> SEQ ID NO: 10
202 <211> LENGTH: 18
203 <212> TYPE: DNA
204 <213> ORGANISM: Homo sapiens
206 <400> SEQUENCE: 10
207 ggggaagcct gaggactg 19
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 19
211 <212> TYPE: DNA
212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 11
215 gattgaaat gtgttccat 19
217 <210> SEQ ID NO: 12
218 <211> LENGTH: 19
219 <212> TYPE: DNA
220 <213> ORGANISM: Homo sapiens
222 <400> SEQUENCE: 12
223 aagggcactc ggtgtgccc 19
225 <210> SEQ ID NO: 13
226 <211> LENGTH: 19
227 <212> TYPE: DNA
228 <213> ORGANISM: Homo sapiens
230 <400> SEQUENCE: 13
231 tctgtctcag ccaataggcg 19
233 <210> SEQ ID NO: 14

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334 <211> LENGTH: 19
335 <212> TYPE: DNA
336 <213> ORGANISM: Homo sapiens
337 <400> SEQUENCE: 14
338 tgggtgaggt cgttcctacg 19
341 <210> SEQ ID NO: 15
342 <211> LENGTH: 19
343 <212> TYPE: DNA
344 <213> ORGANISM: Homo sapiens
345 <400> SEQUENCE: 15
346 gaagacatga tcttcctccc 19
347 <210> SEQ ID NO: 16
348 <211> LENGTH: 19
349 <212> TYPE: DNA
350 <213> ORGANISM: Homo sapiens
351 <400> SEQUENCE: 16
352 caggtccctgt gaaagagg 19
353 <210> SEQ ID NO: 17
354 <211> LENGTH: 19
355 <212> TYPE: DNA
356 <213> ORGANISM: Homo sapiens
357 <400> SEQUENCE: 17
358 cggccctctc gccagggcc 19
359 <210> SEQ ID NO: 18
360 <211> LENGTH: 19
361 <212> TYPE: DNA
362 <213> ORGANISM: Homo sapiens
363 <400> SEQUENCE: 18
364 ccaacagcaga cgggccttc 19
365 <210> SEQ ID NO: 19
366 <211> LENGTH: 19
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
369 <400> SEQUENCE: 19
370 cggcatgata aacatctc 18
371 <210> SEQ ID NO: 20
372 <211> LENGTH: 18
373 <212> TYPE: DNA
374 <213> ORGANISM: Homo sapiens
375 <400> SEQUENCE: 20
376 ttgatccgtg cccccccg 18
377 <210> SEQ ID NO: 21
378 <211> LENGTH: 19
379 <212> TYPE: DNA
380 <213> ORGANISM: Homo sapiens
381 <400> SEQUENCE: 21
382 cctccccarg qttccattac 19
383 <210> SEQ ID NO: 22
384 <211> LENGTH: 19

```

VERIFICATION SUMMARY

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